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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:17:08 ; Search time 10 Seconds
(without alignments)
112.542 Million cell updates/sec

Title: US-09-664-326-23
Perfect score: 368
Sequence: 1 LVTYDCTESGONLCLCGSN.....PKQSHNDGFEEIPEYLQ 65

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 109717 seqs, 17314136 residues
Total number of hits satisfying chosen parameters: 109717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match length	ID	Description
1	368	100.0	65	9 US-09-899-235-15	Sequence 15, Appl
2	113.5	30.8	73	10 US-09-779-054-12	Sequence 12, Appl
3	77	20.9	14	10 US-09-765-614B-29	Sequence 29, Appl
4	77	20.9	14	10 US-09-925-715-25	Sequence 25, Appl
5	77	20.9	15	10 US-09-765-614B-18	Sequence 18, Appl
6	77	20.9	15	10 US-09-925-715-18	Sequence 18, Appl
7	70	19.0	160	10 US-09-798-042-100	Sequence 100, Appl
8	70	19.0	323	10 US-09-159-469-9	Sequence 9, Appl
9	70	19.0	323	10 US-09-798-042-85	Sequence 9, Appl
10	70	19.0	658	10 US-09-798-042-85	Sequence 85, Appl
11	70	19.0	658	10 US-09-798-042-93	Sequence 93, Appl
12	69	18.8	315	9 US-09-808-602-65	Sequence 65, Appl
13	68.5	18.1	1218	10 US-09-853-722-7	Sequence 7, Appl
14	66.5	18.1	810	10 US-09-976-165-34	Sequence 34, Appl
15	66	17.9	197	12 US-10-040-916-6	Sequence 6, Appl
16	64	17.4	18	10 US-09-905-831-5	Sequence 5, Appl
17	64	17.4	51	12 US-10-006-252A-75	Sequence 75, Appl
18	64	17.4	379	10 US-09-864-761-43222	Sequence 43222, A
19	63.5	17.3	568	10 US-09-945-676-7	Sequence 7, Appl

20	63.5	17.3	1036	10 US-09-995-593A-6	Sequence 6, Appl
21	63.5	17.3	1187	10 US-09-995-593A-7	Sequence 7, Appl
22	63.5	17.3	1218	10 US-09-995-593A-11	Sequence 11, Appl
23	63.5	17.3	1218	10 US-09-944-849-3	Sequence 3, Appl
24	63	17.1	51	12 US-10-006-252A-11	Sequence 11, Appl
25	63	17.1	51	12 US-10-006-252A-72	Sequence 72, Appl
26	63	17.1	51	12 US-10-006-252A-73	Sequence 73, Appl
27	63	17.1	51	12 US-10-006-252A-74	Sequence 74, Appl
28	63	17.1	2211	9 US-10-096-961-1	Sequence 1, Appl
29	62.5	17.0	3907	9 US-10-029-217A-24	Sequence 24, Appl
30	62	16.8	50	10 US-09-732-561-20	Sequence 20, Appl
31	62	16.8	50	12 US-10-006-252A-10	Sequence 10, Appl
32	62	16.8	50	12 US-10-006-252A-67	Sequence 67, Appl
33	62	16.8	50	12 US-10-006-252A-68	Sequence 68, Appl
34	62	16.8	50	12 US-10-006-252A-69	Sequence 69, Appl
35	62	16.8	51	10 US-09-732-561-18	Sequence 18, Appl
36	62	16.8	80	10 US-09-732-561-16	Sequence 16, Appl
37	62	16.8	80	10 US-09-732-561-22	Sequence 22, Appl
38	62	16.8	176	9 US-10-024-599-4	Sequence 4, Appl
39	61.5	16.7	513	10 US-09-742-684-2	Sequence 2, Appl
40	61.5	16.7	1604	10 US-09-888-615-73	Sequence 73, Appl
41	61	16.6	690	9 US-09-905-291A-49	Sequence 49, Appl
42	61	16.6	690	9 US-09-902-853-49	Sequence 49, Appl
43	61	16.6	690	10 US-09-828-366-7	Sequence 7, Appl
44	61	16.6	690	10 US-09-909-320-49	Sequence 49, Appl
45	61	16.6	690	10 US-09-909-088B-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-09-899-235-15
; Sequence 15, Application US/09899235
; Patent No. US20020173620A1
; GENERAL INFORMATION:
; APPLICANT: HABERMANN, PAUL
; TITLE OF INVENTION: BIFUNCTIONAL FUSION PROTEINS FORMED FROM HIRUDIN AND
; FILE REFERENCE: 02481.1750-00
; CURRENT APPLICATION NUMBER: US/09/899,235
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Amino acid
; OTHER INFORMATION: Sequence of Refludan (Lau - hirudin)
US-09-899-235-15

Query Match 100.0%; Score 368; DB 9; Length 65;
Best Local Similarity 100.0%; Pred. No. 9.6e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVTYDCTESGONLCLCGSNVCGGNGKCIIGSDDEKNQCVTGEETPKQSHNDGFEEIP 60
DB 1 LVTYDCTESGONLCLCGSNVCGGNGKCIIGSDDEKNQCVTGEETPKQSHNDGFEEIP 60
QY 61 EEYLQ 65
DB 61 EEYLQ 65
RESULT 2
US-09-779-054-12
; Sequence 12, Application US/09779054
; Patent No. US20020120102A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Xinyi
; APPLICANT: Kakkar, Vijay

```
; TITLE OF INVENTION: USE OF DENDROASPIN AS A SCAFFOLD FOR NON-DENDROASPIN DOMAINS
; FILE REFERENCE: A-70312/TAL/AMS
; CURRENT APPLICATION NUMBER: US/09/779,054
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: GB 0002625.2
; PRIOR FILING DATE: 2000-02-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Modified dendroaspin (KGDM-dendroaspin-Hr)
US-09-779-054-12

Query Match          30.8%; Score 113.5; DB 10; Length 73;
Best Local Similarity 64.7%; Pred. No. 9.5e-06;
Matches 22; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 39 CYTGSGT-----PKPSHNDGDEEIPPEYLQ 65
      1 1 : 1 : |||||
DB 40 CFTPKGDMGPGYCFRPSHNDGDEEIPPEYLQ 73

RESULT 3
US-09-765-614B-29
; Sequence 29, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Thrombus
; OTHER INFORMATION: binding peptide
US-09-765-614B-29

Query Match          20.9%; Score 77; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 NDGDFEEIPPEYLQ 65
      |||||
DB 1 NDGDFEEIPPEYLQ 14

RESULT 4
US-09-925-715-25
; Sequence 25, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 14
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Thrombus
; OTHER INFORMATION: binding peptide
US-09-925-715-25

Query Match          20.9%; Score 77; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 NDGDFEEIPPEYLQ 65
      |||||
DB 1 NDGDFEEIPPEYLQ 14

RESULT 5
US-09-765-614B-18
; Sequence 18, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Lipopeptide
; OTHER INFORMATION: with affinity for thrombi
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Dipalmitoyl-Lys
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: AMIDATION
US-09-765-614B-18

Query Match          20.9%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 NDGDFEEIPPEYLQ 65
      |||||
DB 2 NDGDFEEIPPEYLQ 15

RESULT 6
US-09-925-715-18
; Sequence 18, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence:Lipopeptide
OTHER INFORMATION: with an affinity for Unimod
NAME/KEY: MOD.RES
LOCATION: (1)
OTHER INFORMATION: Dipalmitoyl-Lysine
NAME/KEY: MOD.RES
LOCATION: (15)
OTHER INFORMATION: AMIDATION
US-09-925-715-18

Query Match      20.9%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 NDGDFEIPPEYIQ 65
DB 2 NDGDFEIPPEYIQ 15

RESULT 7
US-09-798-042-100
Sequence 100, Application US/09798042
Patent No. US20020068343A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
FILE REFERENCE: 210121.439C7
CURRENT APPLICATION NUMBER: US/09/798,042
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 100
LENGTH: 160
TYPE: PRF
ORGANISM: Ehrlichia sp.
US-09-798-042-100

Query Match      19.0%; Score 70; DB 10; Length 160;
Best Local Similarity 29.6%; Pred. No. 0.88;
Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESGONLCLEGSNVCQGN-----KCLIGSGDEKN-OCVTGEGTPKPSHNDGDF-- 56
DB 79 CGDNGSSTTTSGTNVSEGVFRDFIRATLKEDGSKNWPSSGTGPKPYTNDNAKAVA 138

QY 57 -----EIPPE 62
DB 139 KDLVQELTPEE 149

RESULT 8
US-09-159-469-9
Sequence 9, Application US/09159469
Patent No. US20020064535A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,469
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/106,582
FILING DATE: 29-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-159-469-9

Query Match      19.0%; Score 70; DB 10; Length 323;
Best Local Similarity 29.6%; Pred. No. 1.9;
Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESGONLCLEGSNVCQGN-----KCLIGSGDEKN-OCVTGEGTPKPSHNDGDF-- 56
DB 185 CGDNGSSTTTSGTNVSEGVFRDFIRATLKEDGSKNWPSSGTGPKPYTNDNAKAVA 244

QY 57 -----EIPPE 62
DB 245 KDLVQELTPEE 255

RESULT 9
US-09-798-042-9
Sequence 9, Application US/09798042
Patent No. US20020068343A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
FILE REFERENCE: 210121.439C7
CURRENT APPLICATION NUMBER: US/09/798,042
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 323
TYPE: PRF
ORGANISM: Ehrlichia sp.
US-09-798-042-9

Query Match      19.0%; Score 70; DB 10; Length 323;
Best Local Similarity 29.6%; Pred. No. 1.9;
Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESGONLCLEGSNVCQGN-----KCLIGSGDEKN-OCVTGEGTPKPSHNDGDF-- 56
DB 185 CGDNGSSTTTSGTNVSEGVFRDFIRATLKEDGSKNWPSSGTGPKPYTNDNAKAVA 244

QY 57 -----EIPPE 62
DB 245 KDLVQELTPEE 255
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RESULT 10
US-09-798-042-85
; Sequence 85, Application US/09798042
; Patent No. US20020068343A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; FILE REFERENCE: 210121.439C7
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of fusion protein containing
; US-09-798-042-85

Query Match          19.0%; Score 70; DB 10; Length 658;
Best Local Similarity 29.6%; Pred. No. 3.9;
Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

OY 6 CTEGONCLCGSNVCGGN-----KCIIGSDGKRN-QCVTGEETPRKPSHNDGDF-- 56
DB 194 CDDNCSSTTTTSGTVSETGVFRDFTIRATLKEDSKNMPSTSSGCTPRPVINDAKAVA 253
OY 57 -----EETPEE 62
DB 254 KDLVDELTPPE 264

RESULT 11
US-09-798-042-93
; Sequence 93, Application US/09798042
; Patent No. US20020068343A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; FILE REFERENCE: 210121.439C7
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Ehrlichia
; US-09-798-042-93

Query Match          19.0%; Score 70; DB 10; Length 658;
Best Local Similarity 29.6%; Pred. No. 3.9;
Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

OY 6 CTEGONCLCGSNVCGGN-----KCIIGSDGKRN-QCVTGEETPRKPSHNDGDF-- 56
DB 194 CDDNCSSTTTTSGTVSETGVFRDFTIRATLKEDSKNMPSTSSGCTPRPVINDAKAVA 253
OY 57 -----EETPEE 62
DB 254 KDLVDELTPPE 264
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RESULT 12
US-09-808-602-65
; Sequence 65, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L.
; APPLICANT: Majumder, Kunud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; FILE REFERENCE: 15966-697 CIP
; CURRENT FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Gallus gallus
; US-09-808-602-65

Query Match          18.8%; Score 69; DB 9; Length 315;
Best Local Similarity 33.3%; Pred. No. 2.3;
Matches 21; Conservative 6; Mismatches 26; Indels 10; Gaps 3;

OY 7 TEGONCLC-----EGSNVCGGNKCLIG-SDEKRNQCVTGEETPRKPSHNDGDFEEI 59
DB 45 TEKGEPTCLIEQCKPRHGRPVCGSNGKTYLHNCELHRDACLIGS--RIQVDYDGHCKEK 101
OY 60 PEE 62
DB 102 KSE 104

RESULT 13
US-09-855-722-7
; Sequence 7, Application US/09855722
; Patent No. US20020049306A1
; GENERAL INFORMATION:
; APPLICANT: Sakano, Sei-ji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT FILING DATE: 2001-05-16
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-855-722-7

Query Match          18.6%; Score 68.5; DB 10; Length 1218;
Best Local Similarity 28.8%; Pred. No. 11;
Matches 23; Conservative 5; Mismatches 23; Indels 29; Gaps 4;

OY 6 CTEGONCLCGS-----NVCGGNKCLIG-----SDGKRNQCVTGEETPRKPS 50
DB 276 CNEPWO--CLCETNMGGLCKDKLDLNYCGTHOPCLNGGTCSTNGTPKPYOCSCEPGISGPN 333
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QY 51 -----HNDGFEE 58
Db 334 EIAEHACLSDPCNHRSSCKE 353

RESULT 14

US-09-976-165-34
; Sequence 34, Application US/09976165
; Patent No. US20020107383A1
; GENERAL INFORMATION:
; APPLICANT: FUJIMURA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASARO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIOUITIN-CONJUGATING ENZYME
; FILE REFERENCE: Q-535399
; CURRENT APPLICATION NUMBER: US/09/976,165
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/565,538
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-165-34

Query Match 18.1%; Score 66.5; DB 10; Length 810;
Best Local Similarity 34.1%; Pred. No. 12;
Matches 14; Conservative 7; Mismatches 9; Indels 11; Gaps 3;

QY 5 DCTESG---ONLC--LCESNVCGGCKCIIIGSDGKNC 39
Db 372 NCSEKDHILPENOCRCYRGHNCABGPKC-----GENSEC 407

RESULT 15
US-10-040-916-6
; Sequence 6, Application US/10040916
; Patent No. US20020146769A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John
; Lavalley, Edward
; Racle, Lisa
; Merberg, David
; Treacy, Maurice
; Evans, Cheryl
; Spaulding, Vilki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; ENCODING THEM

NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,916
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,029
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 08/686,878
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-040-916-6

Query Match 17.9%; Score 66; DB 12; Length 197;
Best Local Similarity 33.3%; Pred. No. 2.9;
Matches 18; Conservative 6; Mismatches 22; Indels 8; Gaps 2;

QY 1 LTYTDCESGONLCICGSGVCGGCKCIIIGSDGKNC-----OCVTGEGTPKP 48
Db 38 VTSTGITEDEGPASCYSGEXCKEG--FAISSESEENGESAMSTVAKEGTNVP 89

Search completed: December 30, 2002, 16:21:06
Job time : 10 secs

